Attachment to paper #6 FOAM

```
### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 01.07.09D

Last logoff:  06aug01 09:53:05
Logon file001 06aug01 14:31:02
KWIC is set to 50.
HILIGHT set on as '*'

File   1:ERIC  1966-2001/Aug 01
       (c) format only 2001 The Dialog Corporation

      Set  Items  Description
      ---  -----  -----------
?b 434, 5, 155
       06aug01 14:31:07 User259980 Session D141.1
            $0.23    0.065 DialUnits File1
     $0.23  Estimated cost File1
     $0.23  Estimated cost this search
     $0.23  Estimated total session cost   0.065 DialUnits


SYSTEM:OS  - DIALOG OneSearch
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
       (c) 1998 Inst for Sci Info
  File   5:Biosis Previews(R)  1969-2001/Jul W5
       (c) 2001 BIOSIS
  File 155:MEDLINE(R)  1966-2001/Aug W4

      Set  Items  Description
      ---  -----  -----------
?s (rapid? or fast? or quick?)(w)grow?(w)(bacteri? or microorganism)
         705225  RAPID?
         334874  FAST?
          64454  QUICK?
        1810517  GROW?
        1642666  BACTERI?
          47912  MICROORGANISM
     S1      88  (RAPID? OR FAST? OR QUICK?)(W)GROW?(W)(BACTERI? OR
                 MICROORGANISM)
?s s1 and (cur? plasmid?)
            88  S1
             0  CUR? PLASMID?
     S2      0  S1 AND (CUR? PLASMID?)
?s si and (cur?(s)plasmid?)
>>>File 5 processing for CUR? stopped at CURVIFORMIS
          47641  SI
        1072229  CUR?
         173649  PLASMID?
           4696  CUR?(S)PLASMID?
     S3      1  SI AND (CUR?(S)PLASMID?)
?s s1 and (lack?(w)plasmid?)
            88  S1
         372643  LACK?
         173649  PLASMID?
             67  LACK?(W)PLASMID?
```

```
      S4         0  S1 AND (LACK?(W)PLASMID?)
 ?s s1 and (cure(w)of(w)plasmid?)
              88  S1
           43989  CURE
               0  OF
          173649  PLASMID?
               0  CURE(W)OF(W)PLASMID?
      S5       0  S1 AND (CURE(W)OF(W)PLASMID?)
 ?s cure?(s)plasmid?
           84734  CURE?
          173649  PLASMID?
      S6    1478  CURE?(S)PLASMID?
 ?s s6 and s1
            1478  S6
              88  S1
      S7       0  S6 AND S1
 ?s s1 and (miss?(s)plasmid?)
              88  S1
          100078  MISS?
          173649  PLASMID?
             881  MISS?(S)PLASMID?
      S8       0  S1 AND (MISS?(S)PLASMID?)
 ?ds

 Set     Items   Description
 S1         88   (RAPID? OR FAST? OR QUICK?)(W)GROW?(W)(BACTERI? OR MICROOR-
             GANISM)
 S2          0   S1 AND (CUR? PLASMID?)
 S3          1   SI AND (CUR?(S)PLASMID?)
 S4          0   S1 AND (LACK?(W)PLASMID?)
 S5          0   S1 AND (CURE(W)OF(W)PLASMID?)
 S6       1478   CURE?(S)PLASMID?
 S7          0   S6 AND S1
 S8          0   S1 AND (MISS?(S)PLASMID?)
 ?logoff
       06aug01 14:36:43 User259980 Session D141.2
            $2.24    0.156 DialUnits File434
     $2.24  Estimated cost File434
            $3.29    0.587 DialUnits File5
     $3.29  Estimated cost File5
            $1.65    0.515 DialUnits File155
     $1.65  Estimated cost File155
            OneSearch, 3 files,  1.259 DialUnits FileOS
     $0.30  TYMNET
     $7.48  Estimated cost this search
     $7.71  Estimated total session cost   1.324 DialUnits


### Status: Signed Off. (6 minutes)
```

```
### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSS?PWZ0bgdt ********
Welcome to DIALOG
### Status: Connected


Dialog level 01.07.09D

Last logoff:  02aug01 09:19:26
Logon file001 06aug01 09:41:54
           *** ANNOUNCEMENT ***
                    ***
--Important Notice to Freelance Authors--
See HELP FREELANCE for more information
                    ***
NEW FILE RELEASED
***EIU Business Magazines (File 622)
***IBISWorld Market Research (File 753)
***Investext PDF Index (File 745)
***Daily and Sunday Telegraph (London) Papers (File 756)
***The Mirror Group Publications (United Kingdom) (File 757)

UPDATING RESUMED
***Delphes European Business (File 481)
***Books In Print (File 470)
                             ***
RELOADED
***Kompass Middle East/Africa/Mediterranean (File 585)
***Kompass Asia/Pacific (File 592)
***Kompass Central/Eastern Europe (File 593)
***Kompass Canada (File 594)

New pricing structure for Pharmaprojects (Files 128/928) from
April 1, 2001. Check Help News128 or Help News928 for further
information.

>>>Get immediate news with Dialog's First Release
   news service.  First Release updates major newswire
   databases within 15 minutes of transmission over the
   wire.  First Release provides full Dialog searchability
   and full-text features.  To search First Release files in
   OneSearch simply BEGIN FIRST for coverage from Dialog's
   broad spectrum of news wires.

     >>> Enter BEGIN HOMEBASE for Dialog Announcements <<<
     >>>    of new databases, price changes, etc.      <<<
                    ****
KWIC is set to 50.
HILIGHT set on as '*'

File   1:ERIC  1966-2001/Aug 01
       (c) format only 2001 The Dialog Corporation

      Set  Items  Description
      ---  -----  -----------
?b 155, 5, 434
       06aug01 09:42:07 User259980 Session D140.1
            $0.25    0.070 DialUnits File1
     $0.25  Estimated cost File1
     $0.01  TYMNET
```

```
     $0.26  Estimated cost this search
     $0.26  Estimated total session cost   0.070 DialUnits


SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2001/Aug W4
  File   5:Biosis Previews(R)  1969-2001/Jul W5
         (c) 2001 BIOSIS
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
         (c) 1998 Inst for Sci Info

      Set  Items  Description
      ---  -----  -----------
?s (fast? or quick? or rapid?)(s)grow?
          334874  FAST?
           64454  QUICK?
          705225  RAPID?
         1810517  GROW?
      S1  115852  (FAST? OR QUICK? OR RAPID?)(S)GROW?
?s s1(s)(microorganism or bacter?)
          115852  S1
           47912  MICROORGANISM
         1658662  BACTER?
      S2    7951  S1(S)(MICROORGANISM OR BACTER?)
?s s2 and lack?(w)plasmid?
            7951  S2
          372643  LACK?
          173649  PLASMID?
              67  LACK?(W)PLASMID?
      S3       2  S2 AND LACK?(W)PLASMID?
?rd
...completed examining records
      S4       2  RD (unique items)
?t/9/all

 4/9/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06723973   91151059   PMID: 1963291
 Role of an energy-dependent efflux pump in plasmid pNE24-mediated
resistance to 14- and 15-membered macrolides in Staphylococcus epidermidis.
  Goldman RC; Capobianco JO
  Anti-Infective Research Division, Abbott Laboratories, Abbott Park,
Illinois 60064-3500.
  Antimicrobial agents and chemotherapy (UNITED STATES)  Oct 1990,  34
 (10)  p1973-80,  ISSN 0066-4804   Journal Code: 6HK
  Languages: ENGLISH
  Document type: Journal Article
  Record type: Completed
  Subfile:   INDEX MEDICUS
  We have elucidated a new mechanism for *bacterial* resistance to the
14-membered macrolides oleandomycin and erythromycin and the 15-membered
macrolide azithromycin. Plasmid pNE24, previously isolated from a clinical
specimen of Staphylococcus epidermidis, was characterized as causing
resistance to 14-membered but not 16-membered macrolides by a mechanism
suggested to involve reduced antibiotic permeation of *bacterial* cells (B.
C. Lampson, W. von David, and J. T. Parisi, Antimicrob. Agents Chemother.
30:653-658, 1986). Our recent investigations have demonstrated that S.
epidermidis 958-2 containing plasmid pNE24 also contains an
energy-dependent macrolide efflux pump which maintains intracellular
antibiotic concentrations below those required for binding to ribosomes.
Thus, when strain 958-2 was pretreated with the inhibitor carbonyl cyanide
m-chlorophenylhydrazone (CCCP), macrolide accumulated at the same rate and
to the same extent as in CCCP-treated or untreated control cells *lacking*
*plasmid* pNE24 (strain 958-1). In contrast, macrolide did not accumulate
in energy-competent strain 958-2 but did accumulate to levels equal to
those of ribosomes immediately following CCCP addition. Furthermore,
intracellular macrolide was excreted and *bacteria* resumed *growth* when
CCCP but not macrolide was removed from the *growth* medium. As expected,
the 16-membered macrolide niddamycin accumulated to the same level in
energy-competent strains 958-1 and 958-2 at the same *rapid* rate.
```

Macrolide incubated with lysates prepared from both strains or recovered from cells of strain 958-2 was unmodified and bound to ribosomes from strains 958-1 and 958-2 with identical affinities and kinetics, thus precluding a role for ribosome or drug alteration in the resistance mechanism.(ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: *Antibiotics, Aminoglycoside--pharmacology--PD; *Antibiotics, Macrolide--pharmacology--PD; *Erythromycin--analogs and derivatives--AA; *Erythromycin--pharmacology--PD; *Plasmids--drug effects--DE; *Staphylococcus epidermidis--drug effects--DE; Antibiotics, Aminoglycoside--metabolism--ME; Antibiotics, Macrolide--metabolism--ME; Azithromycin; Carbonyl Cyanide m-Chlorophenyl Hydrazone--pharmacology--PD; Cells, Cultured; Erythromycin--metabolism--ME; Microbial Sensitivity Tests; Ribosomes--metabolism--ME; Staphylococcus epidermidis--growth and development--GD; Structure-Activity Relationship

CAS Registry No.: 0 (Antibiotics, Aminoglycoside); 0 (Antibiotics, Macrolide); 0 (Plasmids); 114-07-8 (Erythromycin); 20283-48-1 (chalcomycin); 20283-69-6 (niddamycin); 555-60-2 (Carbonyl Cyanide m-Chlorophenyl Hydrazone); 83905-01-5 (Azithromycin)

Record Date Created: 19910404

4/9/2 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07353058 BIOSIS NO.: 000090131963
ROLE OF AN ENERGY-DEPENDENT EFFLUX PUMP IN PLASMID PNE-24-MEDIATED RESISTANCE TO 14 MEMBERED MACROLIDES AND 15-MEMBERED MACROLIDES IN STAPHYLOCOCCUS-EPIDERMIDIS

AUTHOR: GOLDMAN R C; CAPOBIANCO J O
AUTHOR ADDRESS: ANTI-INFECTIVE RES. DIV., ABBOTT LAB., ABBOTT PARK, ILL. 60064-3500.

JOURNAL: ANTIMICROB AGENTS CHEMOTHER 34 (10). 1990. 1973-1980. 1990
FULL JOURNAL NAME: Antimicrobial Agents and Chemotherapy
CODEN: AMACC
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: We have elucidated a new mechanism for *bacterial* resistance to the 14-membered macrolides oleandomycin and erythromycin and the 15-membered macrolide azithromycin. Plasmid pNE24, previously isolated from a clinical specimen of Staphylococcus epidermidis, was characterized as causing resistance to 14-membered but not 16-membered macrolides by a mechanism suggested to involve reduced antibiotic permeation of *bacterial* cells (B. C. Lampson, W. von David, and J. T. Parisi, Antimicrob. Agents Chemother. 30:653-658, 1986). Our recent investigations have demonstrated that S. epidermidis 958-2 containing plasmid pNE24 also contains an energy-dependent macrolide efflux pump which maintains intracellular antibiotic concentrations below those required for binding to ribosomes. Thus, when strain 958-2 was pretreated with the inhibitor carbonyl cyanide m-chlorophenylhydrazone (CCCP), macrolide accumulated at the same rate and to the same extent as in CCCP-treated or untreated control cells *lacking* *plasmid* pNE24 (strain 058-1). In contrast, macrolide did not accumulate in energy-competent strain 958-2 but did accumulate to levels equal to those of ribosomes immediately following CCCP addition. Furthermore, intracellular macrolide was excreted and *bacteria* resumed *growth* when CCCP but not macrolide was removed from the *growth* medium. As expected, the 16-membered macrolide niddamycin accumulated to the same level in energy-competent strains 958-1 and 958-2 at the same *rapid* rate. Macrolide incubated with lysates prepared from both strains or recovered from cells of strain 058-2 was unmodified and bound to ribosomes from strains 958-1 and 958-2 with identical affinities and kinetics, thus precluding a role for ribosome or drug alteration in the resistance mechanism. We conclude that the presence of plasmid pNE24 results in specific energy-dependent efflux of 14- and 15-membered macrolides.

DESCRIPTORS: OLEANDOMYCIN ERYTHROMYCIN AZITHROMYCIN ANTIBACTERIAL-DRUG CARBONYL CYANIDE M-CHLOROPHENYLHYDRAZONE
CONCEPT CODES:
10508 Biophysics-Membrane Phenomena

12512 Pathology, General and Miscellaneous-Therapy (1971-)
13002 Metabolism-General Metabolism; Metabolic Pathways
30500 Morphology and Cytology of Bacteria
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
32000 Microbiological Apparatus, Methods and Media
36002 Medical and Clinical Microbiology-Bacteriology
38504 Chemotherapy-Antibacterial Agents
10060 Biochemical Studies-General
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10506 Biophysics-Molecular Properties and Macromolecules
BIOSYSTEMATIC CODES:
05510 Micrococcaceae (1979-)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
Microorganisms
Bacteria
?s (rapid? or quick? or fast?)(w)grow?(w)(bacter? or microorganism)
705225 RAPID?
64454 QUICK?
334874 FAST?
1810517 GROW?
1658662 BACTER?
47912 MICROORGANISM
S5 88 (RAPID? OR QUICK? OR FAST?)(W)GROW?(W)(BACTER? OR MICROORGANISM)
?rd
...examined 50 records (50)
...completed examining records
S6 70 RD (unique items)
?t/9/1-5

6/9/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11426595 21332564 PMID: 11439101
Determination of the chemical structure of the capsular polysaccharide of strain B33, a fast-growing soya bean-nodulating bacterium isolated from an arid region of China.
Rodriguez-Carvajal MA; Tejero-Mateo P; Espartero JL; Ruiz-Sainz JE; Buendia-Claveria AM; Ollero FJ; Yang SS; Gil-Serrano AM
Departamento de Quimica Organica, Facultad de Quimica, Universidad de Sevilla, 41071-Sevilla, Spain.
Biochemical journal (England) Jul 15 2001, 357 (Pt 2) p505-11, ISSN 0264-6021 Journal Code: 9YO
Languages: ENGLISH
Document type: Journal Article
Record type: In Process
Subfile: INDEX MEDICUS
We have determined the structure of a polysaccharide from strain B33, a *fast*-*growing* *bacterium* that forms nitrogen-fixing nodules with Asiatic and American soya bean cultivars. On the basis of monosaccharide analysis, methylation analysis, one-dimensional (1)H- and (13)C-NMR and two-dimensional NMR experiments, the structure was shown to consist of a polymer having the repeating unit -->6)-4-O-methyl-alpha-D-Glcp-(1-->4)-3-O-methyl-beta-D-GlcpA-(1--> (where GlcpA is glucopyranuronic acid and Glcp is glucopyranose). Strain B33 produces a K-antigen polysaccharide repeating unit that does not have the structural motif sugar-Kdx [where Kdx is 3-deoxy-D-manno-2-octulosonic acid (Kdo) or a Kdo-related acid] proposed for different Sinorhizobium fredii strains, all of them being effective with Asiatic soya bean cultivars but unable to form nitrogen-fixing nodules with American soya bean cultivars. Instead, it resembles the K-antigen of S. fredii strain HH303 (rhamnose, galacturonic acid)(n), which is also effective with both groups of soya bean cultivars. Only the capsular polysaccharide from strains B33 and HH303 have monosaccharide components that are also present in the surface polysaccharide of Bradyrhizobium elkanii strains, which consists of a 4-O-methyl-D-glucurono-L-rhamnan.
Record Date Created: 20010705

6/9/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10513685 20120541 PMID: 10653754
Bacterial activity in the rhizosphere analyzed at the single-cell level by monitoring ribosome contents and synthesis rates.
Ramos C; Molbak L; Molin S
Department of Microbiology, The Technical University of Denmark, DK-2800 Lyngby, Denmark.
Applied and environmental microbiology (UNITED STATES) Feb 2000, 66 (2) p801-9, ISSN 0099-2240 Journal Code: 6K6
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
The growth activity of Pseudomonas putida cells colonizing the rhizosphere of barley seedlings was estimated at the single-cell level by monitoring ribosomal contents and synthesis rates. Ribosomal synthesis was monitored by using a system comprising a fusion of the ribosomal Escherichia coli rrnBP1 promoter to a gene encoding an unstable variant of the green fluorescent protein (Gfp). Gfp expression in a P. putida strain carrying this system inserted into the chromosome was strongly dependent on the growth phase and growth rate of the strain, and cells growing exponentially at rates of > or = 0.17 h(-1) emitted growth rate-dependent green fluorescence detectable at the single-cell level. The single-cell ribosomal contents were very heterogeneous, as determined by quantitative hybridization with fluorescently labeled rRNA probes in P. putida cells extracted from the rhizosphere of 1-day-old barley seedlings grown under sterile conditions. After this, cells extracted from the root system had ribosomal contents similar to those found in starved cells. There was a significant decrease in the ribosomal content of P. putida cells when bacteria were introduced into nonsterile bulk or rhizosphere soil, and the Gfp monitoring system was not induced in cells extracted from either of the two soil systems. The monitoring system used permitted nondestructive in situ detection of *fast*-*growing* *bacterial* microcolonies on the sloughing root sheath cells of 1- and 2-day-old barley seedlings grown under sterile conditions, which demonstrated that it may be possible to use the unstable Gfp marker for studies of transient gene expression in plant-microbe systems.
Tags: Support, Non-U.S. Gov't
Descriptors: *Barley--microbiology--MI; *Plant Roots--microbiology--MI; *Pseudomonas putida--genetics--GE; *Pseudomonas putida --growth and development--GD; *RNA, Bacterial--metabolism--ME; *RNA, Ribosomal --metabolism--ME; Colony Count, Microbial; Gene Expression Regulation, Bacterial; Luminescent Proteins--genetics--GE; Luminescent Proteins --metabolism--ME; Microscopy, Confocal; Microscopy, Fluorescence; Promoter Regions (Genetics); RNA Probes; RNA, Bacterial--genetics--GE; RNA, Ribosomal--genetics--GE; Ribosomes--genetics--GE; Ribosomes--metabolism --ME; Soil Microbiology
CAS Registry No.: 0 (Luminescent Proteins); 0 (RNA Probes); 0 (RNA, Bacterial); 0 (RNA, Ribosomal); 147336-22-9 (green fluorescent protein)
Record Date Created: 20000313

6/9/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10503332 20119755 PMID: 10654259
Gene expression, amino acid conservation, and hydrophobicity are the main factors shaping codon preferences in Mycobacterium tuberculosis and Mycobacterium leprae.
de Miranda AB; Alvarez-Valin F; Jabbari K; Degrave WM; Bernardi G
Departamento de Bioquimica e Biologia Molecular, Instituto Oswaldo Cruz, Fundacao Oswaldo Cruz, Rio de Janeiro, Brazil. antonio@gene.dbbm.fiocruz.br
Journal of molecular evolution (UNITED STATES) Jan 2000, 50 (1) p45-55, ISSN 0022-2844 Journal Code: J76
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Mycobacterium tuberculosis and Mycobacterium leprae are the ethiological agents of tuberculosis and leprosy, respectively. After performing extensive comparisons between genes from these two GC-rich bacterial

species, we were able to construct a set of 275 homologous genes. Since these two bacterial species also have a very low growth rate, translational selection could not be so determinant in their codon preferences as it is in other *fast*-*growing* *bacteria*. Indeed, principal-components analysis of codon usage from this set of homologous genes revealed that the codon choices in M. tuberculosis and M. leprae are correlated not only with compositional constraints and translational selection, but also with the degree of amino acid conservation and the hydrophobicity of the encoded proteins. Finally, significant correlations were found between GC3 and synonymous distances as well as between synonymous and nonsynonymous distances.

Tags: Support, Non-U.S. Gov't

Descriptors: *Codon--genetics--GE; *Mycobacterium leprae--genetics--GE; *Mycobacterium tuberculosis--genetics--GE; Amino Acid Sequence; Base Pairing; Conserved Sequence; Evolution, Molecular; Gene Expression Regulation, Bacterial; Nucleotides--genetics--GE; Variation (Genetics)

CAS Registry No.: 0 (Codon); 0 (Nucleotides)

Record Date Created: 20000307

6/9/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10492658 20088834 PMID: 10620682

The gene encoding mycobacterial DNA-binding protein I (MDPI) transformed *rapidly* *growing* *bacteria* to slowly growing bacteria.

Matsumoto S; Furugen M; Yukitake H; Yamada T

Oral Bacteriology, Nagasaki University, School of Dentistry, Sakamoto 1-7-1, Nagasaki, Japan.

FEMS microbiology letters (NETHERLANDS) Jan 15 2000, 182 (2) p297-301, ISSN 0378-1097 Journal Code: FML

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Pathogenic species of Mycobacterium are slowly growing intracellular bacteria. Slow growth is important for the parasitism of these organisms and chronicity of the disease, but its precise mechanism has not been elucidated. Recently, we found that a novel DNA-binding protein (MDPI) was expressed (7-10% in total protein) in mycobacteria, such as Mycobacterium bovis bacillus Calmette-Guerin, Mycobacterium tuberculosis, and Mycobacterium leprae. In this study, we observed that MDPI interfered with replication, transcription, and translation in the analysis in in vitro E. coli cell-free macromolecular biosynthesizing systems. Furthermore, MDPI inhibited the rapid growth of both Escherichia coli and Mycobacterium smegmatis, and NH(2)-terminal second amino acid, asparagine, was observed to be important in terms of this function. These data suggest an important role of MDPI for suppression of growth rates of mycobacteria.

Descriptors: *DNA-Binding Proteins--genetics--GE; *DNA-Binding Proteins --physiology--PH; *Mycobacterium--genetics--GE; *Mycobacterium--growth and development--GD; DNA, Bacterial--biosynthesis--BI; Escherichia coli --genetics--GE; Escherichia coli--metabolism--ME; Gene Expression Regulation, Bacterial; Mycobacterium--metabolism--ME; Transcription, Genetic; Transformation, Bacterial; Translation, Genetic

CAS Registry No.: 0 (DNA, Bacterial); 0 (DNA-Binding Proteins); 0 (MDP1 protein)

Record Date Created: 20000302

6/9/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10239042 99370013 PMID: 10438946

Anergy, IFN-gamma production, and apoptosis in terminal infection of mice with Mycobacterium avium.

Gilbertson B; Zhong J; Cheers C

Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria, Australia.

Journal of immunology (UNITED STATES) Aug 15 1999, 163 (4) p2073-80, ISSN 0022-1767 Journal Code: IFB

Languages: ENGLISH

Document type: Journal Article
Record type: Completed
Subfile: AIM; INDEX MEDICUS

We have followed the course of experimental infection of mice with Mycobacterium avium over an extended period, assessing bacterial numbers and T cell responsiveness. When mice were infected intranasally, bacteria spread to the spleen and liver, but remained in highest numbers in the lungs. Both CD4+ and CD8+ T cells, assayed at any time from 6-28 wk after infection, produced IFN-gamma. After initial *rapid* *growth*, *bacterial* numbers slowly increased from approximately 107 at 6 wk to more than 5 x 108 at 28 wk, indicating that the resistance mechanisms so generated were not adequate to contain the infection. During infection, apoptosis of both CD4+ and CD8+ T cells, measured immediately ex vivo by staining with Annexin V, increased steadily. With some individual exceptions, there was a close correlation between apoptosis of CD4+ cells and level of IFN-gamma production by cultured spleen cells. By 34 wk postinfection, there was an abrupt cessation of IFN-gamma production. No IL-4 was detected, ruling out a switch to Th2 profile. Subsequently, bacterial numbers increased still further to >5 x 109 per lung, and the mice lost body weight and would have died if not killed for experimental or humane reasons. The possibility that T cells exposed over this prolonged period to extremely high doses of Ag may become tolerant by a process of terminal differentiation is discussed.

Tags: Animal; Female; Human; Support, Non-U.S. Gov't

Descriptors: *Apoptosis--immunology--IM; *Clonal Anergy--immunology--IM; *Interferon Type II--biosynthesis--BI; *Mycobacterium avium--immunology--IM; *Tuberculosis--immunology--IM; *Tuberculosis--mortality--MO; Disease Progression; Lung--microbiology--MI; Lung--pathology--PA; Mice; Mice, Inbred C57BL; Spleen--immunology--IM; Spleen--pathology--PA; T-Lymphocytes--immunology--IM; T-Lymphocytes--pathology--PA; Tuberculosis--pathology--PA; Tuberculosis--physiopathology--PP

CAS Registry No.: 82115-62-6 (Interferon Type II)

Record Date Created: 19990909

?t/9/6-20

6/9/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09656208 98125676 PMID: 9464400

Size-selective predation on groundwater bacteria by nanoflagellates in an organic-contaminated aquifer.

Kinner NE; Harvey RW; Blakeslee K; Novarino G; Meeker LD

Environmental Research Group, University of New Hampshire, Durham 03824, USA. nek@christa.unh.edu

Applied and environmental microbiology (UNITED STATES) Feb 1998, 64 (2) p618-25, ISSN 0099-2240 Journal Code: 6K6

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Time series incubations were conducted to provide estimates for the size selectivities and rates of protistan grazing that may be occurring in a sandy, contaminated aquifer. The experiments involved four size classes of fluorescently labeled groundwater bacteria (FLB) and 2- to 3-microns-long nanoflagellates, primarily Spumella guttula (Ehrenberg) Kent, that were isolated from contaminated aquifer sediments (Cape Cod, Mass.). The greatest uptake and clearance rates (0.77 bacteria.flagellate-1.h-1 and 1.4 nl.flagellate-1.h-1, respectively) were observed for 0.8- to 1.5-microns-long FLB (0.21-microns3 average cell volume), which represent the *fastest* *growing* *bacteria* within the pore fluids of the contaminated aquifer sediments. The 19:1 to 67:1 volume ratios of nanoflagellate predators to preferred bacterial prey were in the lower end of the range commonly reported for other aquatic habitats. The grazing data suggest that the aquifer nanoflagellates can consume as much as 12 to 74% of the unattached bacterial community in 1 day and are likely to have a substantive effect upon bacterial degradation of organic groundwater contaminants.

Tags: Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacteria--isolation and purification--IP; *Flagella--physiology--PH; *Water Microbiology; Fluorescence; Fresh Water

Record Date Created: 19980226

6/9/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09359602 97342719 PMID: 9199416
Increased intracellular survival of Mycobacterium smegmatis containing the Mycobacterium leprae thioredoxin-thioredoxin reductase gene.
Wieles B; Ottenhoff TH; Steenwijk TM; Franken KL; de Vries RR; Langermans JA
Department of Immunohematology and Blood Bank, Leiden University Hospital, The Netherlands. Wieles@imm.unibe.ch
Infection and immunity (UNITED STATES) Jul 1997, 65 (7) p2537-41, ISSN 0019-9567 Journal Code: GO7
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
The thioredoxin (Trx) system of Mycobacterium leprae is expressed as a single hybrid protein containing thioredoxin reductase (TR) at its N terminus and Trx at its C terminus. This hybrid Trx system is unique to M. leprae, since in all other organisms studied to date, including other mycobacteria, both TR and Trx are expressed as two separate proteins. Because Trx has been shown to scavenge reactive oxygen species, we have investigated whether the TR-Trx gene product can inhibit oxygen-dependent killing of mycobacteria by human mononuclear phagocytes and as such could contribute to mycobacterial virulence. The gene encoding M. leprae TR-Trx was cloned into the apathogenic, *fast*-*growing* *bacterium* Mycobacterium smegmatis. Recombinant M. smegmatis containing the gene encoding TR-Trx was killed to a significantly lesser extent than M. smegmatis containing the identical vector with either no insert or a control M. leprae construct unrelated to TR-Trx. Upon phagocytosis, M. smegmatis was shown to be killed predominantly by oxygen-dependent macrophage-killing mechanisms. Coinfection of M. smegmatis expressing the gene encoding TR-Trx together with Staphylococcus aureus, which is known to be killed via oxygen-dependent microbicidal mechanisms, revealed that the TR-Trx gene product interferes with the intracellular killing of this bacterium. A similar coinfection with Streptococcus pyogenes, known to be killed by oxygen-independent mechanisms, showed that the TR-Trx gene product did not influence the oxygen-independent killing pathway. The data obtained in this study suggest that the Trx system of M. leprae can inhibit oxygen-dependent killing of intracellular bacteria and thus may represent one of the mechanisms by which M. leprae can deal with oxidative stress within human mononuclear phagocytes.
Tags: Support, Non-U.S. Gov't
Descriptors: *Bacterial Proteins--genetics--GE; *Mycobacterium--genetics--GE; *Mycobacterium--physiology--PH; *Mycobacterium leprae--genetics--GE; *Thioredoxin--genetics--GE; *Thioredoxin Reductase (NADPH)--genetics--GE; Bacterial Proteins--physiology--PH; Genes, Bacterial; Mycobacterium--pathogenicity--PY; Mycobacterium leprae--physiology--PH; Phagocytes--physiology--PH; Recombination, Genetic
CAS Registry No.: 0 (Bacterial Proteins); 0 (thioredoxin-thioredoxin reductase hybrid protein); 52500-60-4 (Thioredoxin)
Enzyme No.: EC 1.6.4.5 (Thioredoxin Reductase (NADPH))
Record Date Created: 19970721

6/9/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08770079 95290491 PMID: 7539631
Guanosine tetraphosphate as a global regulator of bacterial RNA synthesis: a model involving RNA polymerase pausing and queuing.
Bremer H; Ehrenberg M
Program in Molecular and Cell Biology, University of Texas at Dallas, Richardson 750831, USA.
Biochimica et biophysica acta (NETHERLANDS) May 17 1995, 1262 (1) p15-36, ISSN 0006-3002 Journal Code: A0W
Languages: ENGLISH
Document type: Journal Article; Review; Review, Tutorial
Record type: Completed
Subfile: INDEX MEDICUS

A recently reported comparison of stable RNA (rRNA, tRNA) and mRNA synthesis rates in ppGpp-synthesizing and ppGpp-deficient (delta relA delta spoT) bacteria has suggested that ppGpp inhibits transcription initiation from stable RNA promoters, as well as synthesis of (bulk) mRNA. Inhibition of stable RNA synthesis occurs mainly during slow growth of bacteria when cytoplasmic levels of ppGpp are high. In contrast, inhibition of mRNA occurs mainly during fast growth when ppGpp levels are low, and it is associated with a partial inactivation of RNA polymerase. To explain these observations it has been proposed that ppGpp causes transcriptional pausing and queuing during the synthesis of mRNA. Polymerase queuing requires high rates of transcription initiation in addition to polymerase pausing, and therefore high concentrations of free RNA polymerase. These conditions are found in *fast* *growing* *bacteria* . Furthermore, the RNA polymerase queues lead to a promoter blocking when RNA polymerase molecules stack up from the pause site back to the (mRNA) promoter. This occurs most frequently at pause sites close to the promoter. Blocking of mRNA promoters diverts RNA polymerase to stable RNA promoters. In this manner ppGpp could indirectly stimulate synthesis of stable RNA at high growth rates. In the present work a mathematical analysis, based on the theory of queuing, is presented and applied to the global control of transcription in bacteria. This model predicts the in vivo distribution of RNA polymerase over stable RNA and mRNA genes for both ppGpp-synthesizing and ppGpp-deficient bacteria in response to different environmental conditions. It also shows how small changes in basal ppGpp concentrations can produce large changes in the rate of stable RNA synthesis. (62 Refs.)

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *DNA-Directed RNA Polymerase--metabolism--ME; *Guanosine Tetraphosphate--physiology--PH; *RNA, Bacterial--biosynthesis--BI; Bacteria --metabolism--ME; Kinetics; Mathematics

CAS Registry No.: 0 (RNA, Bacterial); 33503-72-9 (Guanosine Tetraphosphate)

Enzyme No.: EC 2.7.7.6 (DNA-Directed RNA Polymerase)

Record Date Created: 19950710

6/9/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08232754 94361317 PMID: 8080143

Expedited detection of drug resistance in tuberculosis patients.

Heifets LB

Department of Microbiology, University of Colorado Health Sciences Center, Denver.

Annals of emergency medicine (UNITED STATES) Sep 1994, 24 (3) p457-61, ISSN 0196-0644 Journal Code: 4Z7

Languages: ENGLISH

Document type: Journal Article; Review; Review, Tutorial

Record type: Completed

Subfile: AIM; INDEX MEDICUS

The increase in disease-causing organisms resistant to standard drug therapy has captured the attention of the medical community and the lay press. Drug resistance in *rapidly* *growing* *bacteria* can be detected within a short period. However, in the case of Mycobacterium tuberculosis, detection may take weeks. This paper examines the current methods available to determine drug susceptibility in M tuberculosis. These laboratory methods can be used as a model to assist the clinician in making rational decisions when managing patients with potentially resistant bacterial infections. (15 Refs.)

Tags: Human

Descriptors: *Microbial Sensitivity Tests--methods--MT; *Tuberculosis, Multidrug-Resistant--diagnosis--DI; *Tuberculosis, Multidrug-Resistant --microbiology--MI; Agar; Antitubercular Agents--therapeutic use--TU; Culture Media; Decision Support Techniques; Diagnosis, Differential; Forecasting; Microbial Sensitivity Tests--trends--TD; Specimen Handling --methods--MT; Time Factors; Tuberculosis, Multidrug-Resistant --drug therapy--DT

CAS Registry No.: 0 (Antitubercular Agents); 0 (Culture Media); 9002-18-0 (Agar)

Record Date Created: 19941005

6/9/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07424055 91333944 PMID: 1870840
Polymorphonuclear leukocytes and bacterial growth of the normal and mildly inflamed conjunctiva.
Ugomori S; Hayasaka S; Setogawa T
Department of Opthalmology, Shimane Medical University, Izumo, Japan.
Ophthalmic research (SWITZERLAND) 1991, 23 (1) p40-4, ISSN 0030-3747 Journal Code: OIE
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
We examined 304 conjunctiva in 152 subjects by clinical, cytologic, and bacteriologic methods. Bacteriologic samples were evaluated after a 48-hour incubation. Bacterial growth was found in 8 (20.5%) of 39 patients with clinically normal conjunctiva and no polymorphonuclear leukocytes (PMNs), and in 8 (61.5%) of 13 subjects with clinically normal conjunctiva and evidence of PMNs. Bacterial growth also was observed in 4 (40.0%) of 10 patients with clinically mild conjunctivitis and no PMNs, in 10 (24.4%) of 41 patients with clinically mild conjunctivitis and a mixture of inflammatory cells or predominantly lymphocytes, and in 37 (75.5%) of 49 patients with clinically mild conjunctivitis and evidence of PMNs. The presence of PMNs was well correlated with the existence of *rapid*-*growing* *bacteria*.
Tags: Female; Human; Male
Descriptors: *Bacteria--growth and development--GD; *Conjunctiva --microbiology--MI; *Conjunctivitis--microbiology--MI; *Conjunctivitis --pathology--PA; *Neutrophils; Adolescence; Adult; Aged; Aged, 80 and over; Child; Child, Preschool; Conjunctiva--cytology--CY; Eye Infections, Bacterial--microbiology--MI; Eye Infections, Bacterial--pathology--PA; Infant; Infant, Newborn; Middle Age
Record Date Created: 19910918

6/9/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07038605 93171246 PMID: 8436584
111Indium labeling of microorganisms to facilitate the investigation of bacterial adhesion.
Ardehali R; Mohammad SF
Artificial Heart Research Laboratory, University of Utah, Salt Lake City 84103.
Journal of biomedical materials research (UNITED STATES) Feb 1993, 27 (2) p269-75, ISSN 0021-9304 Journal Code: HJJ
Contract/Grant No.: HL 42555, HL, NHLBI
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
The ability of bacteria to adhere to polymeric interfaces has attracted considerable attention in recent years. Metabolic labeling of microorganisms with 35S-methionine or other beta-emitters is commonly utilized for quantification of bacterial adhesion to biopolymers. Since the use of these isotopes is cumbersome, the possibility of labeling the microorganisms with 111Indium, a strong gamma-emitter, was explored. This report demonstrates that bacteria can be easily labeled with 111Indium. Staphylococcus aureus, Staphylococcus epidermiids, and Pseudomonas aeruginosa were labeled with either 111Indium-oxine or 35S-methionine; and labeling efficiency, retention of incorporated labels, and growth kinetics of labeled bacteria were compared under identical experimental conditions. Bacteria labeled with 111In-oxine incorporated approximately 90% of radioactivity within 10 min, whereas 35S-methionine incorporation required many hours of incubation. Both the incorporated isotopes were gradually released by *rapidly* *growing* *bacteria* into the suspension medium. Of the total incorporated labels, approximately 20% 111In and 15% 35S were released in the surrounding medium every 24 h. No release of incorporated labels occurred when cells were fixed with 2.5% buffered glutaraldehyde. Growth kinetics and scanning or transmission electron microscopic analysis

showed no detectable differences among control (nonlabeled), 111In-, or 35S-labeled bacteria. Labeling of bacteria with 111In-oxine does not interfere with bacterial adherence. These observations suggest that 111In incorporation provides a simple and rapid method of labeling of microorganisms. Compared to currently available techniques, the use of 111In-labeled bacteria will facilitate the quantitation of adherent bacteria to interfaces.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacterial Adhesion--physiology--PH; *Indium Radioisotopes --diagnostic use--DU; Bacteria--growth and development--GD; Bacteria --physiology--PH; Cell Division; Isotope Labeling; Methionine--metabolism --ME; Microscopy, Electron; Microscopy, Electron, Scanning; Oxyquinoline --metabolism--ME; Polymers; Sulfur Radioisotopes--diagnostic use--DU

CAS Registry No.: 0 (Indium Radioisotopes); 0 (Polymers); 0 (Sulfur Radioisotopes); 148-24-3 (Oxyquinoline); 7005-18-7 (Methionine)

Record Date Created: 19930322

6/9/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06889927 93007487 PMID: 1393818

Cooperation between two Thiobacillus strains for heavy-metal removal from municipal sludge.

Blais JF; Auclair JC; Tyagi RD

Institut national de la recherche scientifique (INRS-EAU), Universite du Quebec, Sainte-Foy, Canada.

Canadian journal of microbiology (CANADA) Mar 1992, 38 (3) p181-7, ISSN 0008-4166 Journal Code: CJ3

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

A mixed culture of two *fast*-*growing* *bacterial* strains for heavy-metal solubilization of municipal sewage sludge has been developed. Strain VA-7 decreases the initial sludge pH (7-8.5) to a value between 4.0 and 4.5. Then, strain VA-4 begins growing and further reduces the pH to values below 2.0. The rapid decrease of sludge pH by a mixed culture through sulfur oxidation into sulfuric acid solubilizes the toxic metals (Cd 83-96%, Cr 16-54%, Cu 85-87%, Mn 91-94%, Ni 78-79%, Pb 28-46%, Zn 82-96%) to levels recommended for intensive use of residual sludge in agriculture. A study of the physiological and metabolic characteristics of these strains revealed that isolate VA-7 is a strain of Thiobacillus thioparus (ATCC 55127), while isolate VA-4 corresponds to a Thiobacillus thiooxidans (ATCC 55128). These bacterial strains possess distinctive physiological characteristics that allow them to easily grow and solubilize heavy metals in municipal sludge.

Tags: Support, Non-U.S. Gov't

Descriptors: *Metals--metabolism--ME; *Sewage; *Thiobacillus--metabolism --ME; Hydrogen-Ion Concentration; Metals--isolation and purification--IP; Solubility; Sulfates--metabolism--ME; Thiobacillus--growth and development --GD; Thiobacillus--isolation and purification--IP

CAS Registry No.: 0 (Metals); 0 (Sulfates)

Record Date Created: 19921120

6/9/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06792377 92046955 PMID: 1942732

[Establishment of a host-vector system in Mycobacterium bovis BCG]

Mizuguchi Y; Taniguchi H; Udou T; Qin MH; Goto Y; Tokunaga T

Department of Microbiology, University of Occupational and Environmental Health, Kitakyushu, Japan.

Kekkaku (JAPAN) Sep 1991, 66 (9) p607-13, ISSN 0022-9776 Journal Code: KUO

Languages: JAPANESE

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

The recombinant plasmids, pYT72 and pYT92, were generated from a

mycobacterial plasmid, pMSC262, and a Escherichia coli plasmid, pACYC177. These plasmids were capable of replication, and of stable maintainance in Mycobacterium bovis BCG when introduced by electroporation technique. Efficiency of transformation was about 10(4) transformants/micrograms DNA, and was the highest in the phage sensitive mutants (S-10, S-20) isolated from BCG Tokyo strain. We have also isolated transformable mutants from *rapidly* *growing* *bacterium*, M. smegmatis strains Jucho and TMC1533. By isolating deletion mutants from pYT72/92, we could determine the location of replication region of pMSC262 within a 2.3 kb Pst I-Hind III fragment. Using this fragment, we constructed "mini" shuttle plasmid pYT937 (5.9 kb in size) which possesses kanamycin and ampicillin resistance markers and replicates in both E. coli and Mycobacterium. Nucleotide sequence analysis of the replication region revealed that there are 2 potential coding regions which contain more than 200 amino acids. The largest one (ORF1) which codes 311 amino acids, however, lacks Shine-Dalgarno like sequence in the upstream and therefore may not be functional. The other coding region (ORF2) contains 260 amino acids and was preceded by Shine-Dalgarno like sequence. Upstream of the ORF2, there were several repeat sequences which may be important in the plasmid replication. GC content of the 2.3 kb fragment was 69.8%.

Descriptors: *Genetic Vectors; *Mycobacterium bovis--genetics--GE; DNA, Recombinant; Plasmids

CAS Registry No.: 0 (DNA, Recombinant); 0 (Genetic Vectors); 0 (Plasmids)

Record Date Created: 19911202

6/9/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06548148 88274019 PMID: 2899112

Evaluation of three disinfectants after in-use stress.

Isenberg HD; Giugliano ER; France K; Alperstein P
Long Island Jewish Medical Center, New Hyde Park, NY 11042.

Journal of hospital infection (ENGLAND) Apr 1988, 11 (3) p278-85, ISSN 0195-6701 Journal Code: ID6

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Solutions of 2.0% and 3.4% glutaraldehyde, and of 0.5% phenate with 0.18% glutaraldehyde were stressed with a microbial and organic soil load for the periods advocated by the respective manufacturers. The disinfecting efficacy of the stressed solutions was challenged with Staphylococcus aureus, Pseudomonas aeruginosa, Bacillus subtilis, Mycobacterium bovis (BCG), a water Mycobacterium sp. and Candida albicans. The three disinfectants were active against the *fast*-*growing* *bacteria* in appropriate dilutions; lesser dilutions of the glutaraldehyde solutions killed the mycobacteria and the yeast, while stressed phenate with glutaraldehyde did not. One hour exposure of the stressed disinfectants failed to kill the spore preparations while reducing the number of survivors.

Tags: Comparative Study

Descriptors: *Aldehydes--pharmacology--PD; *Disinfectants--standards--ST; *Drug Contamination; *Glutaral--pharmacology--PD; Bacteria--drug effects --DE; Candida albicans--drug effects--DE; Drug Evaluation; Glutaral --administration and dosage--AD

CAS Registry No.: 0 (Aldehydes); 0 (Disinfectants); 111-30-8 (Glutaral)

Record Date Created: 19880819

6/9/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06538119 88197403 PMID: 3283039

New developments in medical microbiology: computer-assisted diagnosis and automated instruments.

Heizmann W; Pickert A; Kloss T; Werner H
Abt. Med. Mikrobiologie, Hygiene-Institut der Universitat, Tubingen.

Infection (GERMANY, WEST) 1988, 16 (1) p69-74, ISSN 0300-8126

Journal Code: GO8
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS

Time and accuracy required for diagnosis are two of the most important factors in medical microbiology. Computer-assisted diagnosis is one tool to overcome these problems. The software of such systems, much more than the hardware, is of utmost importance and both have to fulfill several items. 1) High flexibility and integration within the already existing working schemes of the laboratory. 2) Terminals in every laboratory. 3) High speed of calculation. 4) Online data transfer from automated instruments. 5) External terminals on intensive care units. 6) Epidemiological and etiopathological investigations have to be possible at any time. In the laboratory the burden of simple, repeating tasks is diminished, inquiries can be made in a minute and precise information about the epidemiological situation can be gained within a few hours. Thus, calculated antimicrobial therapy depending on the incidence of certain pathogens in given specimens in different departments is possible. In the case of *fast*-*growing* *bacteria*, preliminary reports, including susceptibility testing available within the first 24 h, are possible and will be of great help to the clinician in monitoring the calculated antimicrobial regimen. External terminals will allow continuous flow of data from the laboratory to wards and vice versa.

Descriptors: *Diagnosis, Computer-Assisted; Autoanalysis--methods--MT; Software; Time Factors
Record Date Created: 19880607

6/9/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06070023 85303428 PMID: 2412407
Use of intrinsic antibiotic resistance for characterisation and identification of rhizobia from nodules of Vigna unguiculata (L) Walp. and Phaseolus vulgaris (L).
Dakora FD
Acta microbiologica Polonica (POLAND) 1985, 34 (2) p187-94, ISSN 0137-1320 Journal Code: 17I
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS

Intrinsic resistance to low concentrations of antibiotics was used to characterise 83 isolates from nodules of cowpea (Vigna unguiculata) and field bean (Phaseolus vulgaris). Characterisation and differentiation of isolates from cowpea was made difficult by associated *fast*-*growing* *bacteria* inside the nodule tissue. Thus, reliable pure culture was difficult to secure without repeated isolation and even via nodulation of the appropriate homologous host. Although the technique may be satisfactory for differentiation and identification of fast-growing rhizobia, it is rated inferior to serology on aspects of facility, time and accuracy where rhizobia from cowpea nodules are concerned. Fingerprint patterns of isolates revealed considerable heterogeneity amongst the populations even where there was commonality of location and/or host plant. Pure cultures of slow-growing rhizobia from V. unguiculata nodules were generally more resistant to the concentrations of antibiotics used than fast-growing nodule bacteria from P. vulgaris.

Tags: Support, Non-U.S. Gov't
Descriptors: *Antibiotics--pharmacology--PD; *Legumes--microbiology--MI; *Rhizobium--classification--CL; Drug Resistance, Microbial; Genotype; Microbial Sensitivity Tests; Rhizobium--drug effects--DE; Rhizobium --isolation and purification--IP
CAS Registry No.: 0 (Antibiotics)
Record Date Created: 19851007

6/9/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05776526 88120383 PMID: 2828768

Bacterial DNA segregation: its motors and positional control.
Cavalier-Smith T
Department of Biophysics, Cell and Molecular Biology, King's College, London, U.K.
Journal of theoretical biology (ENGLAND) Aug 7 1987, 127 (3) p361-72, ISSN 0022-5193 Journal Code: K8N
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS

A model for DNA segregation in bacteria is proposed which involves not merely growth of the cell membrane and wall, as previously assumed, but also the active movement of one of the two chromosome sister origins by a DNA helicase enzyme and of the chromosome termini and the bulk of the chromosomes by supercoiling tension exerted by DNA gyrase. This provides a unified mechanism for DNA chromosome movement in prosthecate budding bacteria as well as for bacteria that undergo binary fission. The positional control of DNA segregation and the plane of cell division depend, I suggest, on four things: (1) the attachment of the daughter chromosome termini to the cell wall in a position adjacent to the new cell poles at about the time of septation, (2) the displacement of the parental chromosome terminus from this attachment site by the mobile origin, which attaches itself instead to the wall at that point, (3) the movement of the chromosome terminus to a new location in between the daughter origins by the tension of supercoiling, and (4) the determination of the location of the future septum at the position occupied by the chromosome terminus at the time of septal initiation; septum-initiation proteins are postulated to achieve this by binding directly or indirectly to the chromosome terminus. This mechanism automatically ensures ordered DNA segregation in *rapidly* *growing* *bacteria* with more than two sister origins of replication.

Tags: Support, Non-U.S. Gov't
Descriptors: *DNA, Bacterial--metabolism--ME; *Models, Biological; Cell Division; Chromosomes, Bacterial--metabolism--ME; DNA Helicases--metabolism--ME; DNA Replication; DNA Topoisomerase (ATP-Hydrolysing)--metabolism--ME
CAS Registry No.: 0 (DNA, Bacterial)
Enzyme No.: EC 3.1.- (DNA Helicase I); EC 5.99.- (DNA Helicases); EC 5.99.1.3 (DNA Topoisomerase (ATP-Hydrolysing))
Record Date Created: 19880318

6/9/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05568788 88283052 PMID: 3293892
Susceptibility testing of Nocardia species for the clinical laboratory.
Wallace RJ; Steele LC
Department of Microbiology, University of Texas Health Center, Tyler 75710.
Diagnostic microbiology and infectious disease (UNITED STATES) Mar 1988, 9 (3) p155-66, ISSN 0732-8893 Journal Code: DMI
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS

Not all patients are able to tolerate or show a favorable response to the treatment of choice for Nocardia, the sulfonamides. Many new drugs are available with good activity against N. asteroides, the most common pathogenic species, although susceptibility to these agents, including amikacin, amoxicillin/clavulanic acid, and the third generation cephalosporins, is variable. For these and other reasons, we recommend routine susceptibility testing of Nocardia. Disk diffusion testing on Mueller Hinton agar is the best currently available clinical method. A suggested control strain and tentative susceptible and resistant breakpoints for 12 antimicrobial agents are provided. This includes agents not previously evaluated, including cefotaxime, amikacin, ciprofloxacin, and doxycycline. The zones of inhibition were all larger than those currently used by the NCCLS for *rapidly* *growing* *bacteria*, and the disk breakpoints generally fit best with the MIC breakpoints used with the dilution susceptibility method (M7-T). A broth microdilution MIC method is described that showed good correlation with disk diffusion results, but need additional study. Because of limited experience in most laboratories

with this species, reliance on a good reference laboratory for confirmatory susceptibility testing is recommended. Beta-lactamase testing is not helpful, as almost all Nocardia produce beta-lactamase, although many isolates retain susceptibility to selected beta-lactams.

Tags: Support, Non-U.S. Gov't

Descriptors: *Microbial Sensitivity Tests--methods--MT; *Nocardia--drug effects--DE; Culture Media; Diffusion; Drug Resistance, Microbial; Laboratories, Hospital; Microbial Sensitivity Tests--standards--ST; Nocardia asteroides--drug effects--DE

CAS Registry No.: 0 (Culture Media)

Record Date Created: 19880908

6/9/19 (Item 19 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05271631 89291105 PMID: 2737778

Endocarditis from a dental focus. Importance of oral hygiene in valvar heart disease.

Verhaaren H; Claeys G; Verschraegen G; de Niel C; Leroy J; Clement D

Department of Paediatrics, University Hospital, Gent State University, Belgium.

International journal of cardiology (NETHERLANDS) Jun 1989, 23 (3) p343-7, ISSN 0167-5273 Journal Code: GQW

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Fastidiously *growing* *bacteria* more and more are recognised as a source of infectious endocarditis. Over recent years, three new cases of endocarditis caused by Actinobacillus actinomycetemcomitans were diagnosed in our institution. The rise in frequency is possibly secondary to better laboratory skills. Two patients with Actinobacillus (Haemophilus) actinomycetemcomitans endocarditis presented the classical history of preexisting valvar disease together with poor dental hygiene. The third patient had no congenital or rheumatic preexisting lesion to the valves. The distal part of a ventriculo-atrial drainage device had caused microtrauma to the tricuspid valve. The right-sided endocarditis in this patient was complicated by pulmonary septic emboli. Dental origin of the infection was very likely in this patient too. No dental procedure had been performed in the months preceding the endocarditis of our three patients. They presented endocarditis with an oral microorganism in the absence of any dental manipulation. All three had very poor dental hygiene. Better dental care could possibly have prevented this serious complication.

Tags: Case Report; Human; Male

Descriptors: *Actinobacillus Infections--etiology--ET; *Endocarditis, Bacterial--etiology--ET; *Heart Valve Diseases--complications--CO; *Oral Hygiene; Actinobacillus Infections--prevention and control--PC; Adult; Aged ; Child; Endocarditis, Bacterial--prevention and control--PC

Record Date Created: 19890810

6/9/20 (Item 20 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04943712 85248541 PMID: 4014276

Pathogenesis of endocarditis.

Sullam PM; Drake TA; Sande MA

American journal of medicine (UNITED STATES) Jun 28 1985, 78 (6B) p110-5, ISSN 0002-9343 Journal Code: 3JU

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: AIM; INDEX MEDICUS

The pathophysiology of infective endocarditis comprises at least three critical elements: preparation of the cardiac valve for bacterial adherence, adhesion of circulating bacteria to the prepared valvular surface, and survival of the adherent bacteria on the surface, with propagation of the infected vegetation. It appears that circulating bacteria do not readily adhere to normal endothelial surfaces. Trauma to the valve, however, produces an alteration in the endothelial cells,

leading to either disruption of the surface and deposition of platelets and fibrin, or other phenomena that render the surface susceptible to colonization by circulating bacteria. Once the surface is prepared, some bacterial strains appear to adhere to the fibrin-platelet matrix more avidly than others. The bacterial virulence factors that promote adherence are complex, but at least one, an extracellular polysaccharide (dextran), has been identified. Adherence can be blocked by antibodies directed against various surface structures. The survival of bacteria adherent to the surface of the vegetation appears to be complex as well, requiring resistance in situ to the bactericidal properties of complement and phagocytosis by white cells. In addition, vegetation propagation involves activation of the clotting cascade. For at least some streptococci, this occurs partly through perturbation of the valvular cells to produce tissue factor (tissue thromboplastin), which results in the deposition and growth of a fibrin-platelet clot over the *rapidly* *growing* *bacterial* colonies.

Tags: Animal; Human

Descriptors: *Endocarditis, Bacterial--etiology--ET; Bacteria--growth and development--GD; Endocardium--microbiology--MI; Heart Valves--microbiology --MI; Septicemia--complications--CO; Thrombosis--complications--CO

Record Date Created: 19850812

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S1	115852	(FAST? OR QUICK? OR RAPID?)(S)GROW?
S2	7951	S1(S)(MICROORGANISM OR BACTER?)
S3	2	S2 AND LACK?(W)PLASMID?
S4	2	RD (unique items)
S5	88	(RAPID? OR QUICK? OR FAST?)(W)GROW?(W)(BACTER? OR MICROORG-ANISM)
S6	70	RD (unique items)

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7/9/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

09359602 97342719 PMID: 9199416

Increased intracellular survival of Mycobacterium smegmatis containing the Mycobacterium leprae thioredoxin-thioredoxin reductase gene.

Wieles B; Ottenhoff TH; Steenwijk TM; Franken KL; de Vries RR; Langermans JA

Department of Immunohematology and Blood Bank, Leiden University Hospital, The Netherlands. Wieles@imm.unibe.ch

Infection and immunity (UNITED STATES) Jul 1997, 65 (7) p2537-41, ISSN 0019-9567 Journal Code: GO7

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

The thioredoxin (Trx) system of Mycobacterium leprae is expressed as a single hybrid protein containing thioredoxin reductase (TR) at its N terminus and Trx at its C terminus. This hybrid Trx system is unique to M. leprae, since in all other organisms studied to date, including other mycobacteria, both TR and Trx are expressed as two separate proteins. Because Trx has been shown to scavenge reactive oxygen species, we have investigated whether the TR-Trx gene product can inhibit oxygen-dependent killing of mycobacteria by human mononuclear phagocytes and as such could contribute to mycobacterial virulence. The gene encoding M. leprae TR-Trx was *cloned* into the apathogenic, *fast*-*growing* *bacterium* Mycobacterium smegmatis. Recombinant M. smegmatis containing the gene encoding TR-Trx was killed to a significantly lesser extent than M. smegmatis containing the identical vector with either no insert or a control M. leprae construct unrelated to TR-Trx. Upon phagocytosis, M. smegmatis was shown to be killed predominantly by oxygen-dependent macrophage-killing mechanisms. Coinfection of M. smegmatis expressing the gene encoding TR-Trx together with Staphylococcus aureus, which is known to be killed via oxygen-dependent microbicidal mechanisms, revealed that the

TR-Trx gene product interferes with the intracellular killing of this bacterium. A similar coinfection with Streptococcus pyogenes, known to be killed by oxygen-independent mechanisms, showed that the TR-Trx gene product did not influence the oxygen-independent killing pathway. The data obtained in this study suggest that the Trx system of M. leprae can inhibit oxygen-dependent killing of intracellular bacteria and thus may represent one of the mechanisms by which M. leprae can deal with oxidative stress within human mononuclear phagocytes.

Tags: Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--genetics--GE; *Mycobacterium--genetics --GE; *Mycobacterium--physiology--PH; *Mycobacterium leprae--genetics--GE; *Thioredoxin--genetics--GE; *Thioredoxin Reductase (NADPH)--genetics--GE; Bacterial Proteins--physiology--PH; Genes, Bacterial; Mycobacterium --pathogenicity--PY; Mycobacterium leprae--physiology--PH; Phagocytes --physiology--PH; Recombination, Genetic

CAS Registry No.: 0 (Bacterial Proteins); 0 (thioredoxin-thioredoxin reductase hybrid protein); 52500-60-4 (Thioredoxin)

Enzyme No.: EC 1.6.4.5 (Thioredoxin Reductase (NADPH))

Record Date Created: 19970721

7/9/2 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11928782 BIOSIS NO.: 199900174891
Regulation and cloning of microbial chitinase genes.
AUTHOR: Felse P A; Panda T(a)
AUTHOR ADDRESS: (a)Biotechnology Research Centre, Indian Institute of Technology-Madras, Chennai, 600 036**India
JOURNAL: Applied Microbiology and Biotechnology 51 (2):p141-151 Feb., 1999
ISSN: 0175-7598
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A range of chitinase genes from microorganisms have been *cloned* and the potential uses of these genetically manipulated organisms are being investigated by various researchers. Fungi and yeast are better producers of chitinase than bacteria. Since fungi grow at a slower rate, there have been efforts to *clone* the fungal chitinase genes into *fast* -*growing* *bacteria*. This review gives a brief survey of recent progress in the regulation and *cloning* of microbial chitinase genes. Emphasis is placed on the post-translational modification and localization of the recombinant protein in the host. Various amino acid domains are present in this protein. The mode of catalytic activity of the recombinant protein in comparison to the wild-type protein is discussed in the available literature. The different mechanisms involved in the regulation of chitinase genes from various microorganisms is discussed by the researchers. The scope of future research and conclusions yet to be obtained in this particular area are also outlined in this review.

REGISTRY NUMBERS: 9001-06-3: CHITINASE; 9001-06-3D: CHITINASES
DESCRIPTORS:
MAJOR CONCEPTS: Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Bacteria--Microorganisms; Fungi--Plantae; Microorganisms
ORGANISMS: bacteria (Bacteria); fungi (Fungi); microorganisms (Microorganisms)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Fungi; Microorganisms; Nonvascular Plants; Plants
CHEMICALS & BIOCHEMICALS: chitinases; proteins
METHODS & EQUIPMENT: gene cloning--molecular genetic method
MISCELLANEOUS TERMS: biotechnology; gene regulation; microbial growth
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
03504 Genetics and Cytogenetics-Plant
10010 Comparative Biochemistry, General
10050 Biochemical Methods-General

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  10060   Biochemical Studies-General
  10300   Replication, Transcription, Translation
  10506   Biophysics-Molecular Properties and Macromolecules
  10802   Enzymes-General and Comparative Studies; Coenzymes
  13002   Metabolism-General Metabolism; Metabolic Pathways
  29500   Microorganisms, General
  31000   Physiology and Biochemistry of Bacteria
  31500   Genetics of Bacteria and Viruses
  32000   Microbiological Apparatus, Methods and Media
  39008   Food and Industrial Microbiology-General and Miscellaneous
  51518   Plant Physiology, Biochemistry and Biophysics-Enzymes
  51519   Plant Physiology, Biochemistry and Biophysics-Metabolism
  51522   Plant Physiology, Biochemistry and Biophysics-Chemical
            Constituents
BIOSYSTEMATIC CODES:
  01000   Microorganisms-Unspecified
  05000   Bacteria-General Unspecified (1992- )
  15000   Fungi-Unspecified
?ds

Set     Items   Description
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S2       7951   S1(S)(MICROORGANISM OR BACTER?)
S3          2   S2 AND LACK?(W)PLASMID?
S4          2   RD (unique items)
S5         88   (RAPID? OR QUICK? OR FAST?)(W)GROW?(W)(BACTER? OR MICROORG-
            ANISM)
S6         70   RD (unique items)
S7          2   S6(S)CLON?
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            $3.30  2 Types
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    $23.09  Estimated cost this search
    $23.35  Estimated total session cost   2.841 DialUnits


### Status: Signed Off. (12 minutes)
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